SUPPLEMENTARY MATERIAL: Heterogeneity of Acute Myeloid Leukemia patients explored through single-cell and single-sample gene regulatory networks

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1 Supplementary Tables

KNN Progenitor				SVM Progenitor			
Class	Precision	Recall	F_1-score	Class	Precision	Recall	F_1-score
AML1012	1.00	0.29	0.45	AML1012	0.11	0.72	0.18
AML328	0.96	0.73	0.83	AML328	1.00	0.12	0.22
AML329	0.29	0.89	0.44	AML329	0.71	0.17	0.28
AML371	1.00	0.11	0.20	AML371	0.96	0.13	0.23
AML419A	1.00	0.10	0.19	AML419A	1.00	0.18	0.31
AML420B	1.00	0.15	0.26	AML420B	0.13	0.13	0.13
AML707B	0.39	0.75	0.51	AML707B	1.00	0.12	0.22
AML870	1.00	0.01	0.03	AML870	0.79	0.13	0.22
AML916	1.00	0.09	0.16	AML916	0.90	0.13	0.23
AML921A	0.16	0.63	0.26	AML921A	0.51	0.20	0.28
BM3	0.98	0.23	0.37	BM3	0.10	0.32	0.16
BM4	0.32	0.77	0.45	BM4	1.00	0.46	0.63
BM5	0.00	0.00	0.00	BM5	0.81	0.15	0.25
Macro avg	0.70	0.37	0.32	Macro avg	0.69	0.23	0.26
Weighted avg	0.70	0.37	0.32	Weighted avg	0.69	0.23	0.26
Accuracy			0.37	Accuracy			0.23

Table 1: Full classification reports for KNN, SVM, and RF classifiers on Progenitor Cells.

RF Progenitor

Class	Precision	Recall	F_1-score
AML1012	1.00	1.00	1.00
AML328	1.00	1.00	1.00
AML329	1.00	1.00	1.00
AML371	1.00	1.00	1.00
AML419A	1.00	1.00	1.00
AML420B	1.00	1.00	1.00
AML707B	1.00	1.00	1.00
AML870	1.00	1.00	1.00
AML916	1.00	1.00	1.00
AML921A	1.00	1.00	1.00
BM3	1.00	1.00	1.00
BM4	1.00	1.00	1.00
BM5	1.00	1.00	1.00
Macro avg	1.00	1.00	1.00
Weighted avg	1.00	1.00	1.00
Accuracy			1.00

KNN Monocyte

Class	Precision	Recall	F_1-score
AML1012	0.15	0.81	0.26
AML210A	0.14	0.49	0.22
AML328	1.00	0.02	0.03
AML371	1.00	0.01	0.02
AML419A	1.00	0.02	0.03
AML556	1.00	0.02	0.03
AML921A	1.00	0.14	0.25
BM4	1.00	0.10	0.18
Macro avg	0.81	0.19	0.13
Weighted avg	0.81	0.19	0.13
Accuracy			0.19

SVM Monocyte

Class	Precision	Recall	F_1-score
AML1012	0.35	0.25	0.29
AML210A	0.13	0.14	0.13
AML328	0.87	0.11	0.20
AML371	0.16	0.81	0.26
AML419A	0.75	0.08	0.14
AML556	1.00	0.10	0.18
AML921A	0.12	0.09	0.10
BM4	0.21	0.20	0.21
Macro avg	0.50	0.21	0.19
Weighted avg	0.50	0.21	0.19
Accuracy			0.21

RF Monocyte

Class	Precision	Recall	F_1-score
AML1012	1.00	1.00	1.00
AML210A	1.00	1.00	1.00
AML328	1.00	1.00	1.00
AML371	1.00	1.00	1.00
AML419A	1.00	1.00	1.00

KNN Dendritic				SVM Dendritic			
Class	Precision	Recall	F_1-score	Class	Precision	Recall	F_1-score
AML1012	1.00	0.04	0.08	AML1012	0.16	0.67	0.26
AML210A	0.15	0.99	0.26	AML210A	0.20	0.31	0.24
AML371	1.00	0.07	0.13	AML371	0.18	0.18	0.18
AML556	1.00	0.07	0.13	AML556	1.00	0.11	0.20
AML921A	1.00	0.10	0.17	AML921A	1.00	0.05	0.09
BM3	0.93	0.53	0.68	BM3	0.18	0.15	0.17
BM4	1.00	0.22	0.37	BM4	1.00	0.06	0.12
Macro avg	0.88	0.27	0.26	Macro avg	0.52	0.20	0.18
Weighted avg	0.88	0.27	0.26	Weighted avg	0.52	0.20	0.18
Accuracy			0.27	Accuracy			0.20

RF Dendritic			
Class	Precision	Recall	F_1-score
AML1012	1.00	1.00	1.00
AML210A	1.00	1.00	1.00
AML371	1.00	1.00	1.00
AML556	1.00	1.00	1.00
AML921A	1.00	1.00	1.00
BM3	1.00	1.00	1.00
BM4	1.00	1.00	1.00
Macro avg	1.00	1.00	1.00
Weighted avg	1.00	1.00	1.00
Accuracy			1.00

Table 3: Classification report comparison for KNN, SVM, and RF classifiers on Dendritic Cells.

Cell Type	KNN				SVM				RF			
	Accuracy	Precision	Recall	F_1-score	Accuracy	Precision	Recall	F_1-score	Accuracy	Precision	Recall	F_1-score
Progenitor	0.37	0.70	0.37	0.32	0.23	0.69	0.23	0.26	1.00	1.00	1.00	1.00
Monocyte	0.19	0.81	0.19	0.13	0.21	0.50	0.21	0.19	1.00	1.00	1.00	1.00
Dendritic	0.27	0.88	0.27	0.26	0.20	0.52	0.20	0.18	1.00	1.00	1.00	1.00

Table 4: Classification accuracy, macro-averaged precision, recall, and F_1-score for each machine learning technique (KNN, SVM, RF) and cell type (Progenitor, Monocyte, Dendritic).

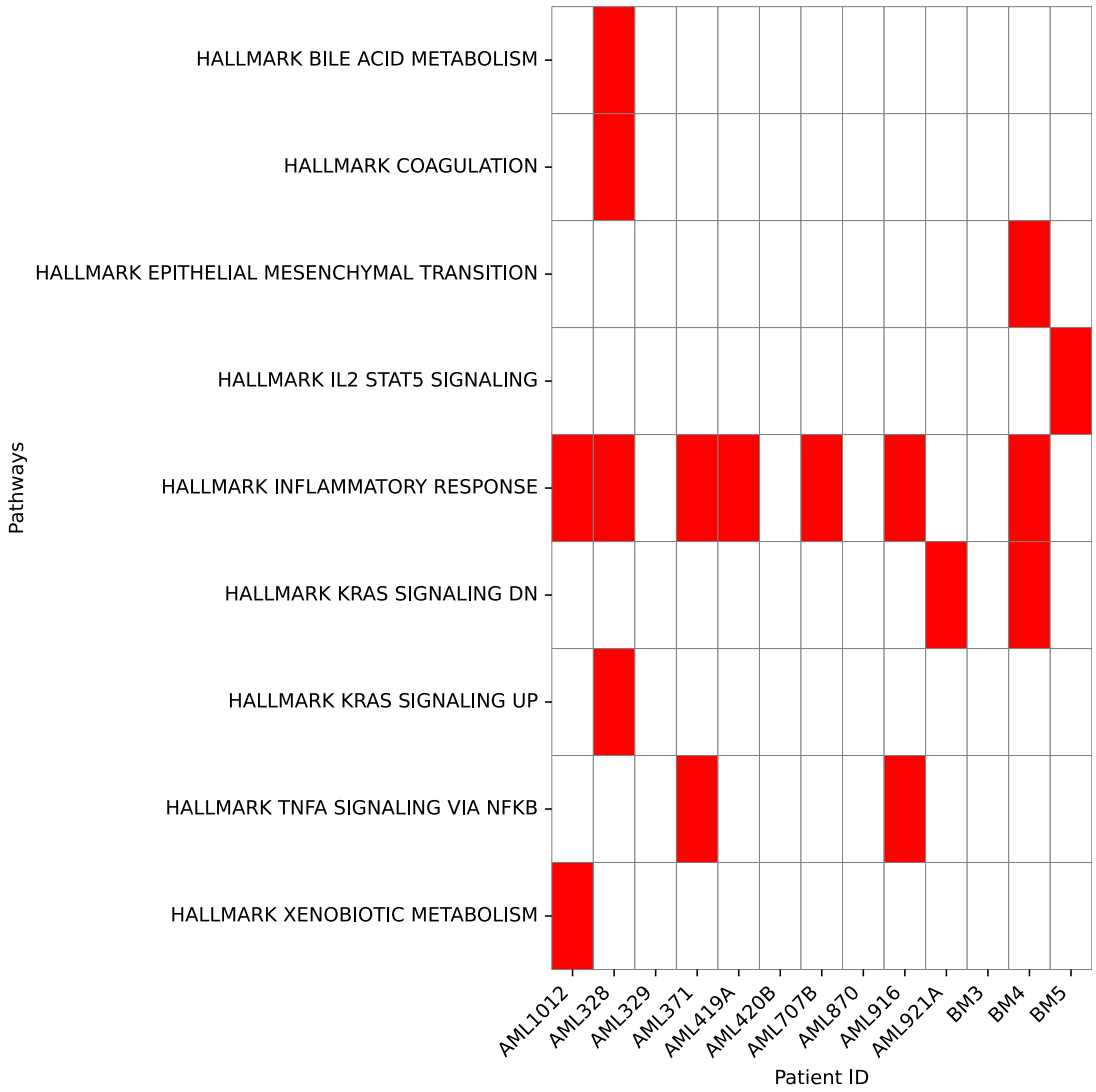

Figure 1: Hallmark Pathway Enrichment of the top 2500 genes by node degree/connections in progenitor cells for different patients. Benjamini-Hochberg correction was specified for multiple testing. Pathways with an adjusted p-value below 0.05 and q-value below 0.2 were considered significantly enriched.

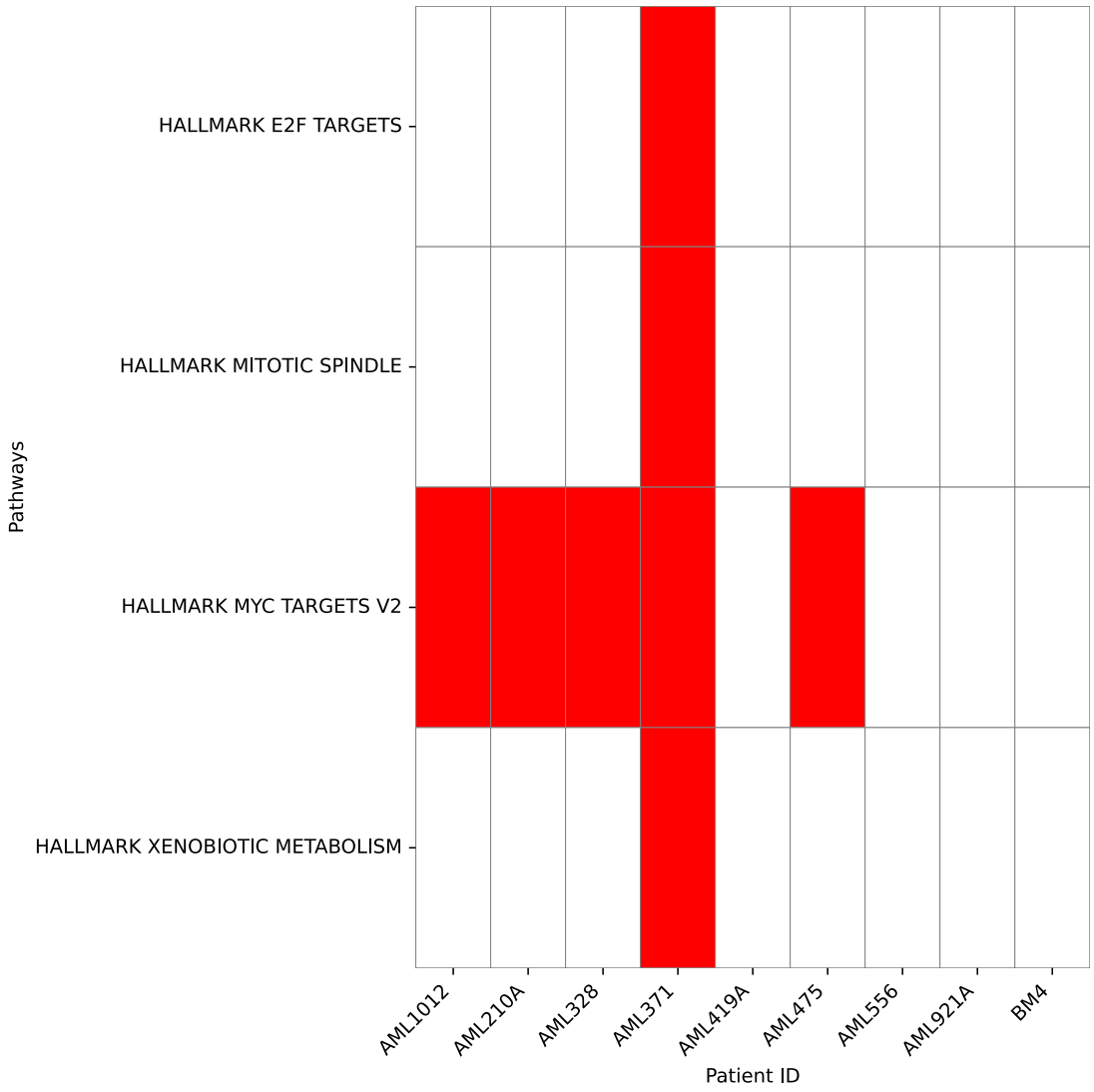

Figure 2: Hallmark Pathway Enrichment of the top 2500 genes by node degree/connections in monocyte cells for different patients. Benjamini-Hochberg correction was specified for multiple testing. Pathways with an adjusted p-value below 0.05 and q-value below 0.2 were considered significantly enriched.

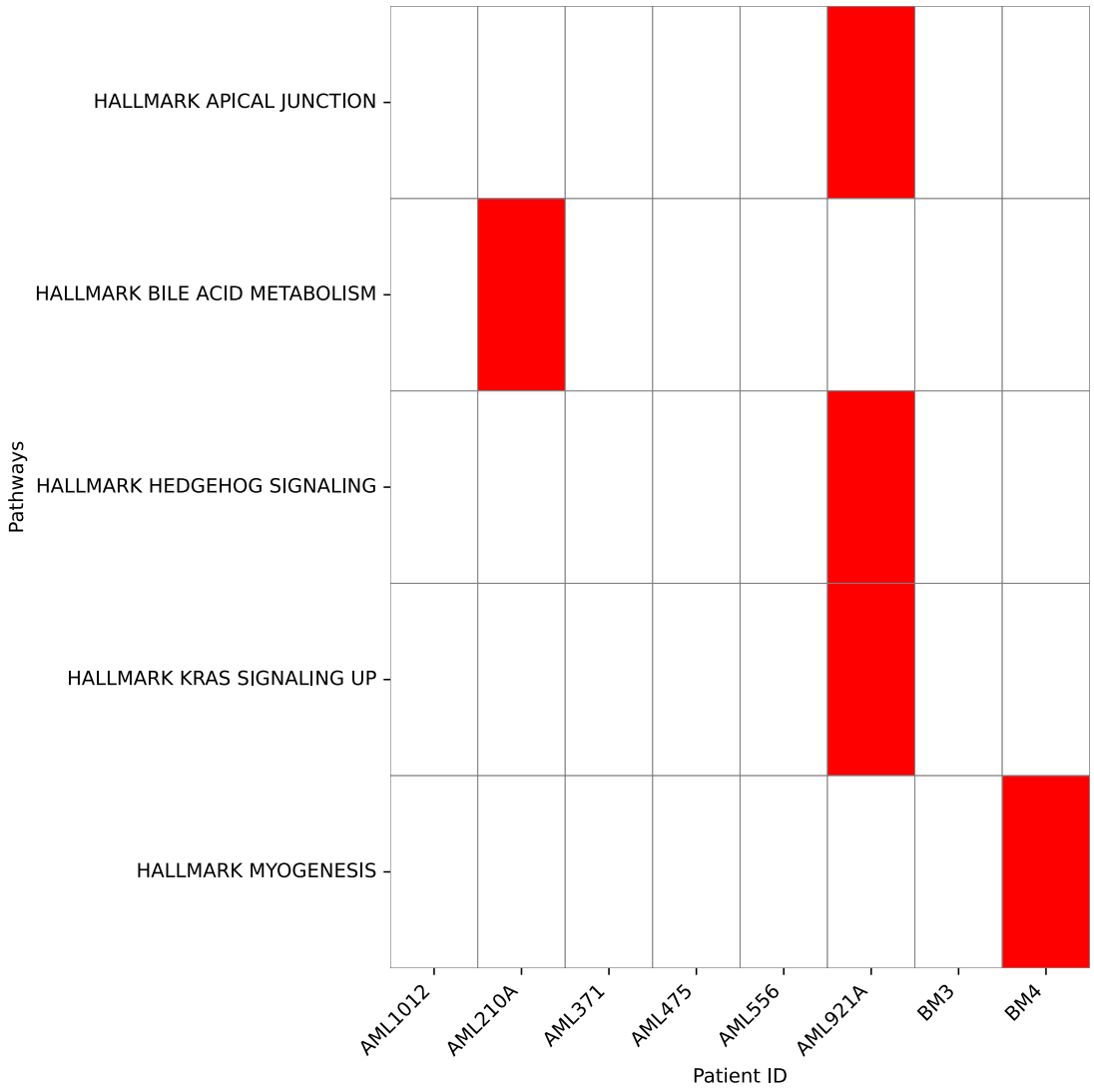

Figure 3: Hallmark Pathway Enrichment of the top 2500 genes by node degree/connections in dendritic cells for different patients. Benjamini-Hochberg correction was specified for multiple testing. Pathways with an adjusted p-value below 0.05 and q-value below 0.2 were considered significantly enriched.

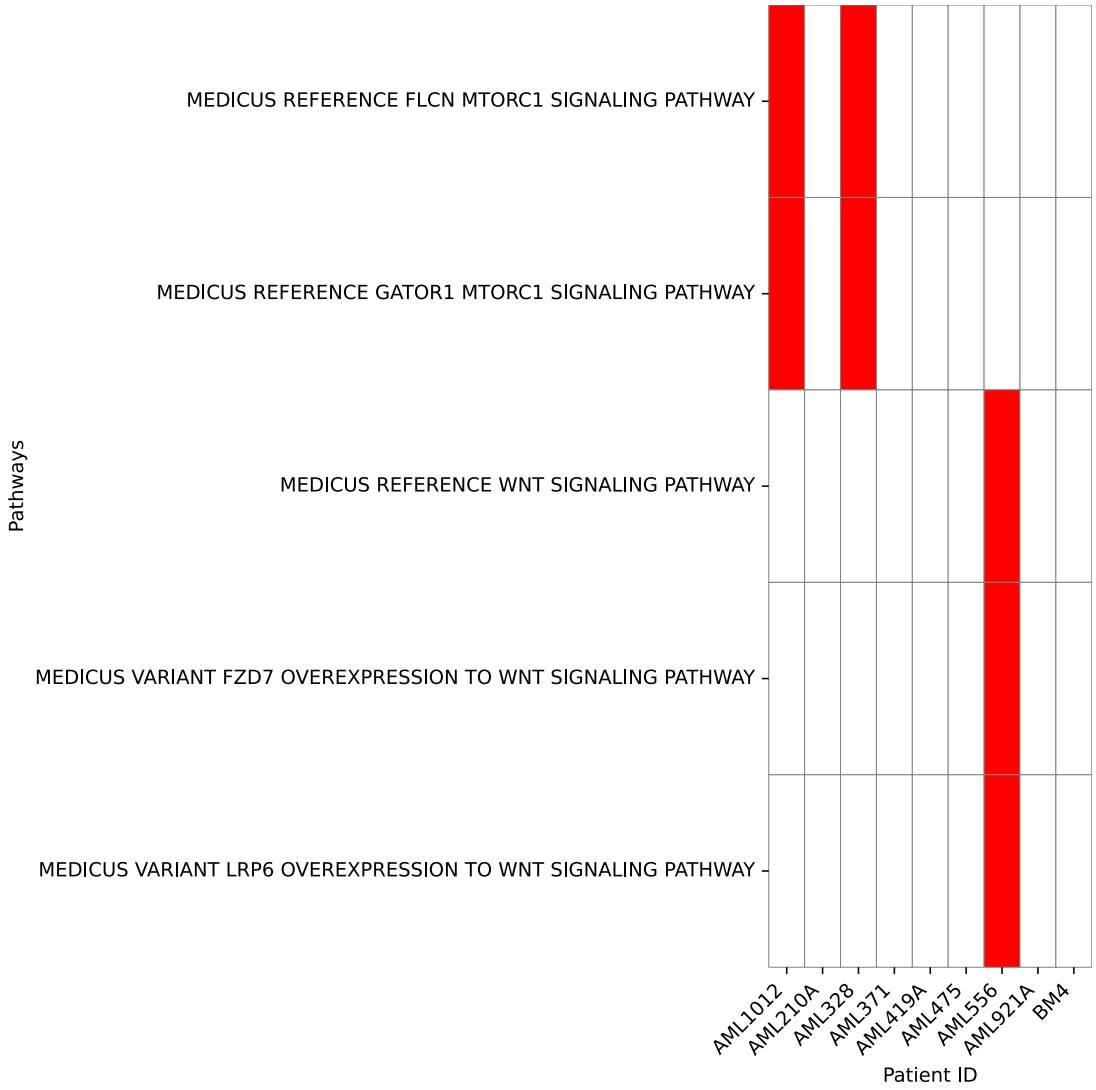

Figure 4: Curated KEGG Canonical Pathway Enrichment of the top 2500 genes by node degree/connections in monocyte cells for different patients. Benjamini-Hochberg correction was specified for multiple testing. Pathways with an adjusted p-value below 0.05 and q-value below 0.2 were considered significantly enriched.

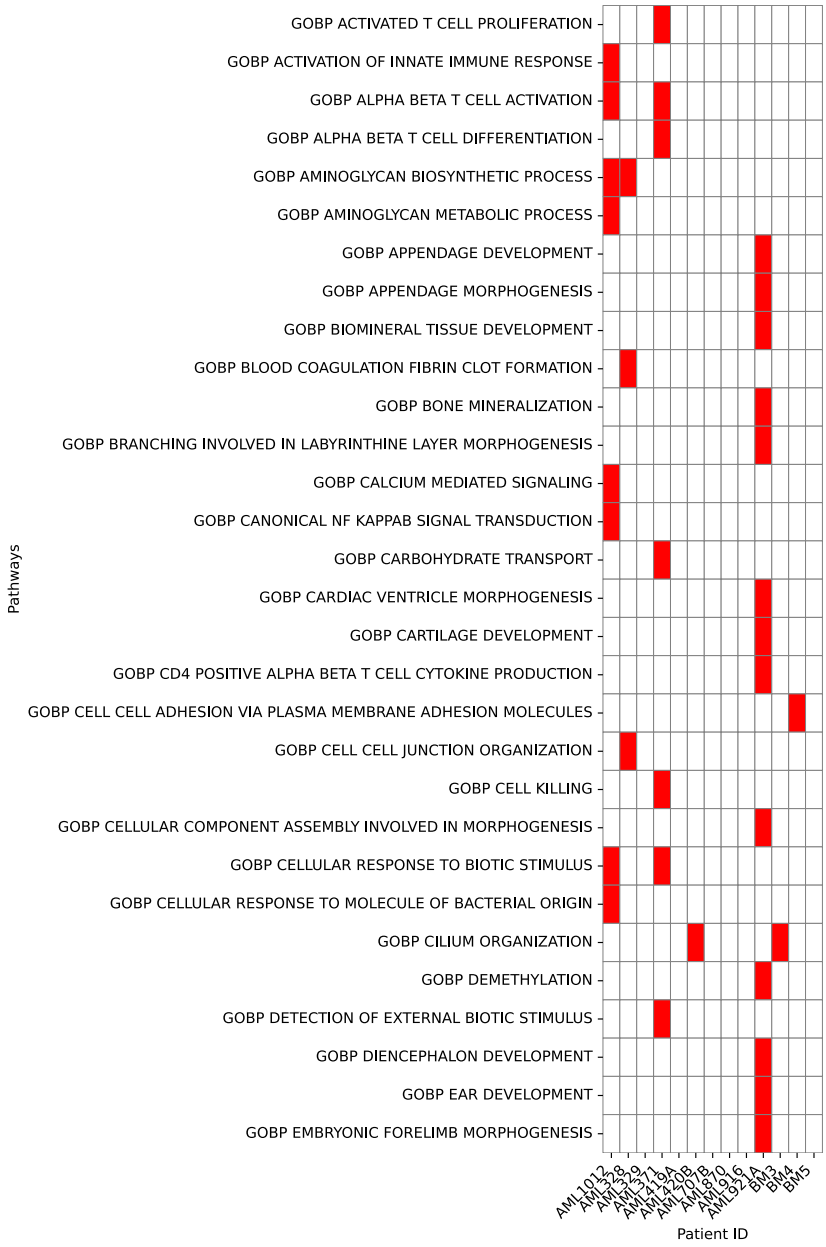

Figure 5: Gene Ontology Biological Process Pathway Enrichment of top 2500 genes by node degree/connections in progenitor cells for different patients (part 1 of 5). Benjamini-Hochberg correction was specified for multiple testing. Pathways with an adjusted p-value below 0.05 and q-value below 0.2 were considered significantly enriched.

Figure 6: Gene Ontology Biological Process Pathway Enrichment of top 2500 genes by node degree/connections in progenitor cells for different patients (part 2 of 5). Benjamini-Hochberg correction was specified for multiple testing. Pathways with an adjusted p-value below 0.05 and q-value below 0.2 were considered significantly enriched.

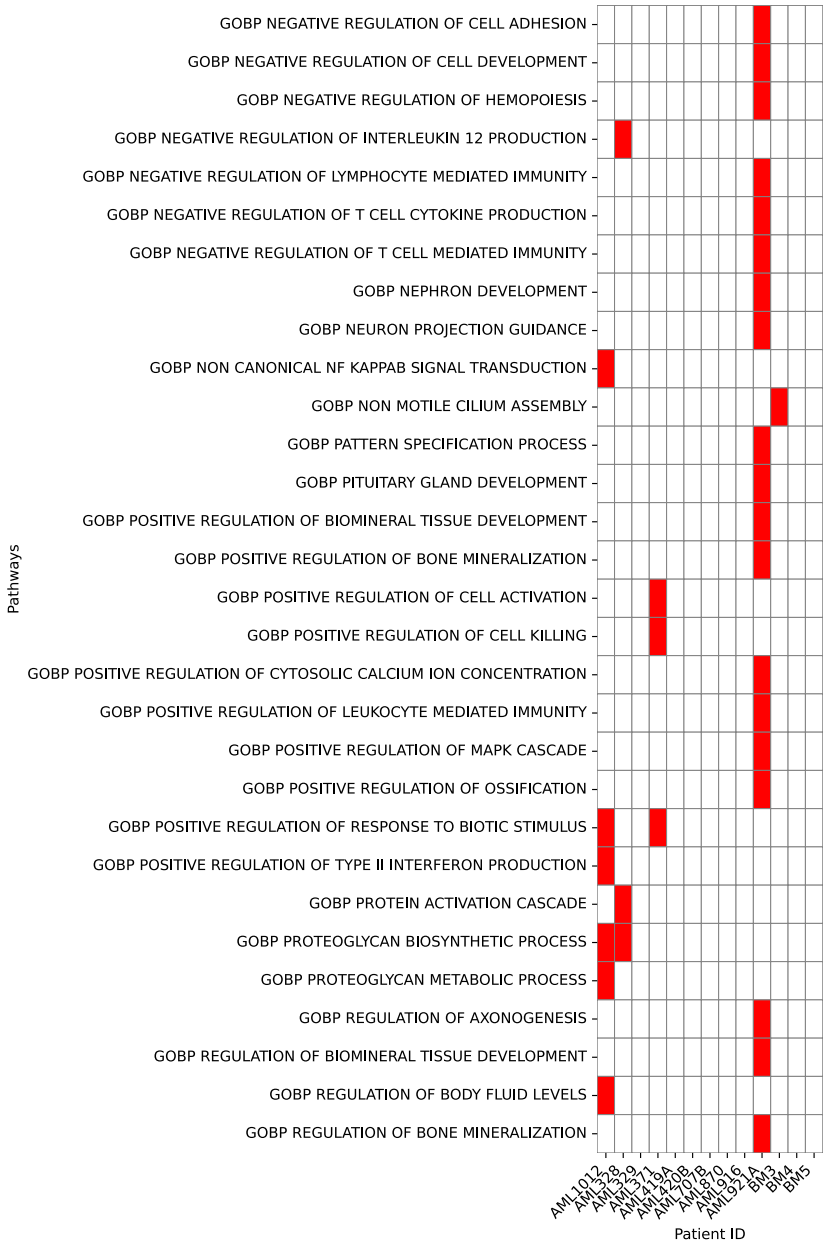

Figure 7: Gene Ontology Biological Process Pathway Enrichment of top 2500 genes by node degree/connections in progenitor cells for different patients (part 3 of 5). Benjamini-Hochberg correction was specified for multiple testing. Pathways with an adjusted p-value below 0.05 and q-value below 0.2 were considered significantly enriched.

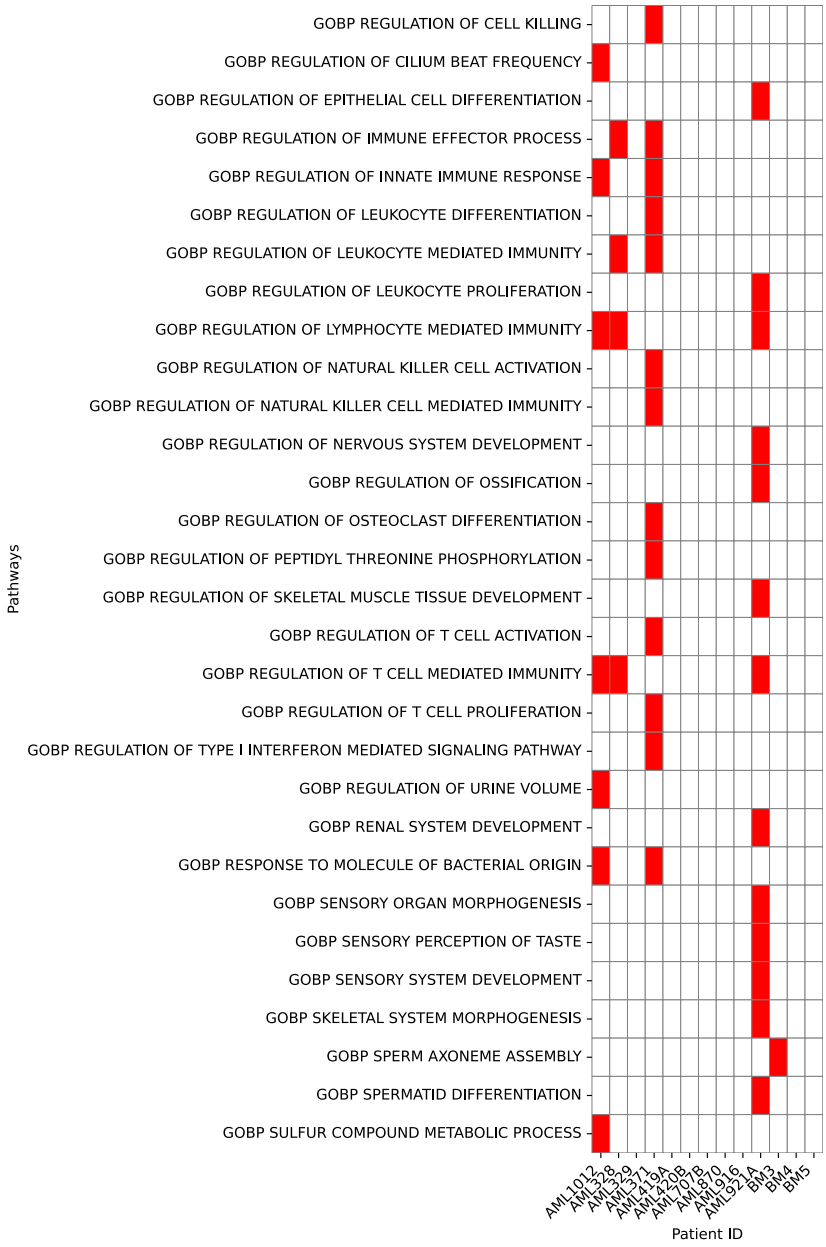

Figure 8: Gene Ontology Biological Process Pathway Enrichment of top 2500 genes by node degree/connections in progenitor cells for different patients (part 4 of 5). Benjamini-Hochberg correction was specified for multiple testing. Pathways with an adjusted p-value below 0.05 and q-value below 0.2 were considered significantly enriched.

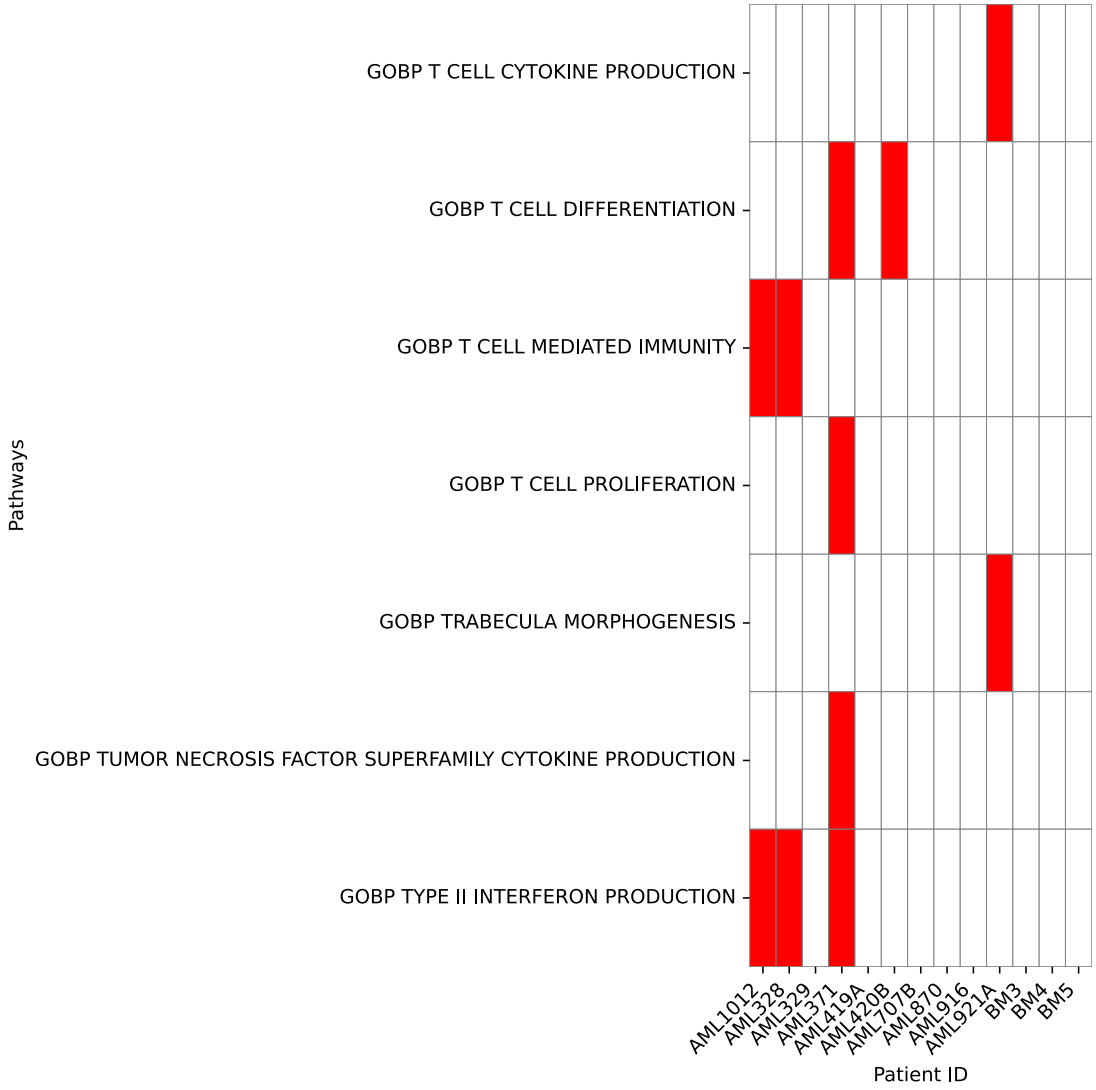

Figure 9: Gene Ontology Biological Process Pathway Enrichment of top 2500 genes by node degree/connections in progenitor cells for different patients (part 5 of 5). Benjamini-Hochberg correction was specified for multiple testing. Pathways with an adjusted p-value below 0.05 and q-value below 0.2 were considered significantly enriched.

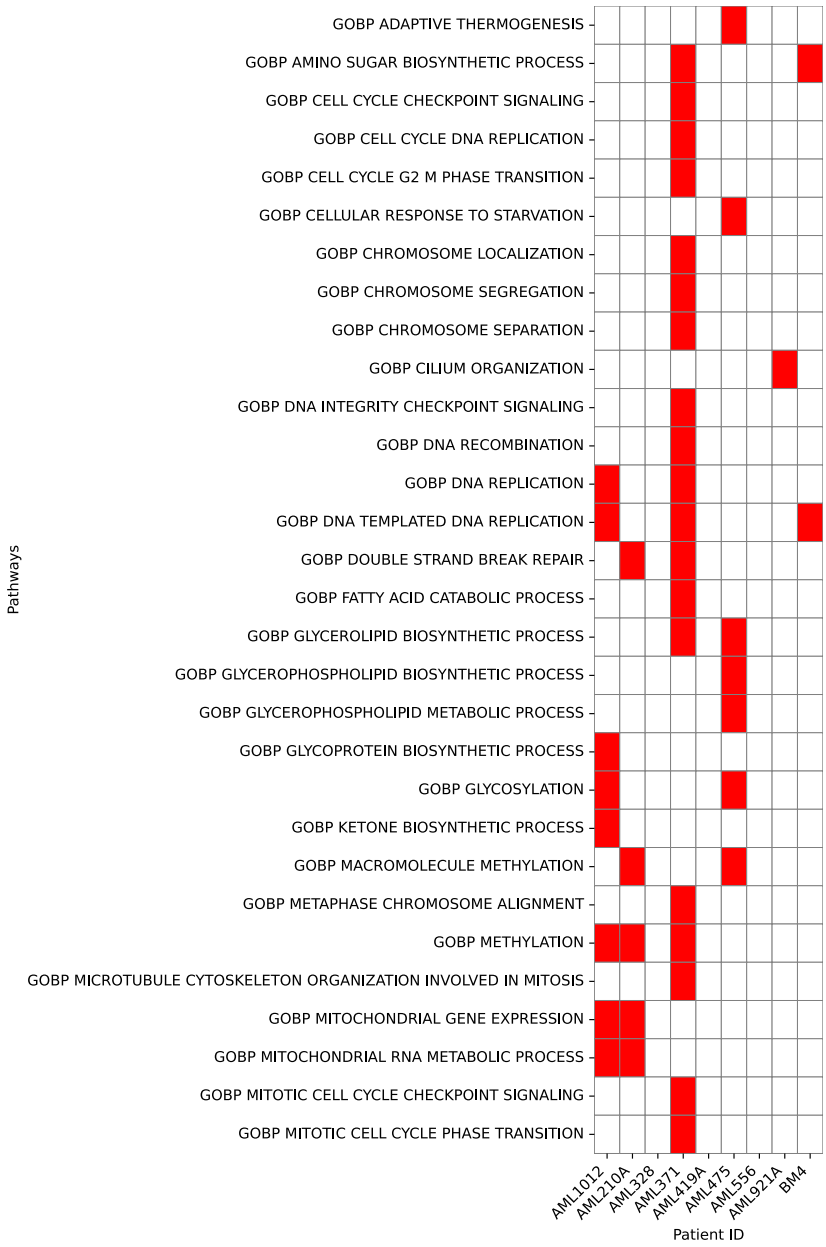

Figure 10: Gene Ontology Biological Process Pathway Enrichment of top 2500 genes by node degree/connections in monocyte cells for different patients (part 1 of 3). Benjamini-Hochberg correction was specified for multiple testing. Pathways with an adjusted p-value below 0.05 and q-value below 0.2 were considered significantly enriched.

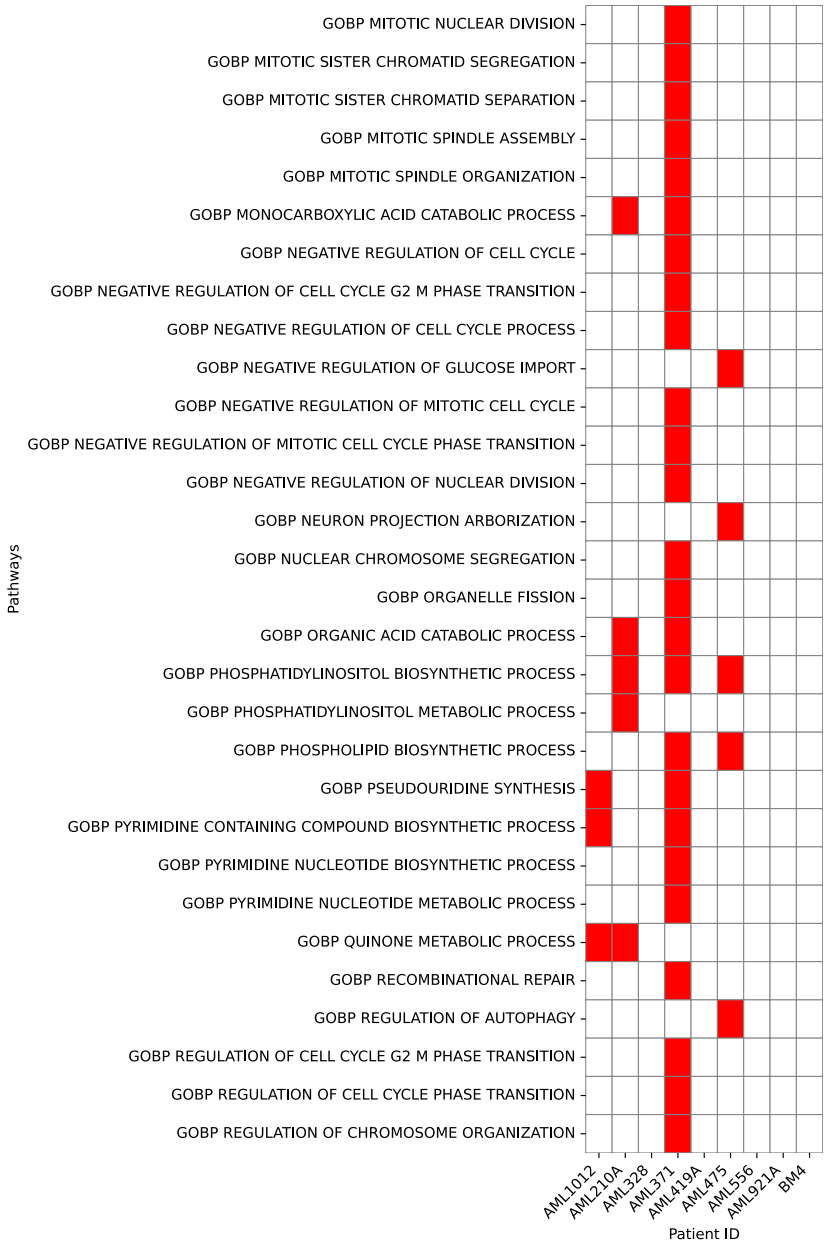

Figure 11: Gene Ontology Biological Process Pathway Enrichment of top 2500 genes by node degree/connections in monocyte cells for different patients (part 2 of 3). Benjamini-Hochberg correction was specified for multiple testing. Pathways with an adjusted p-value below 0.05 and q-value below 0.2 were considered significantly enriched.

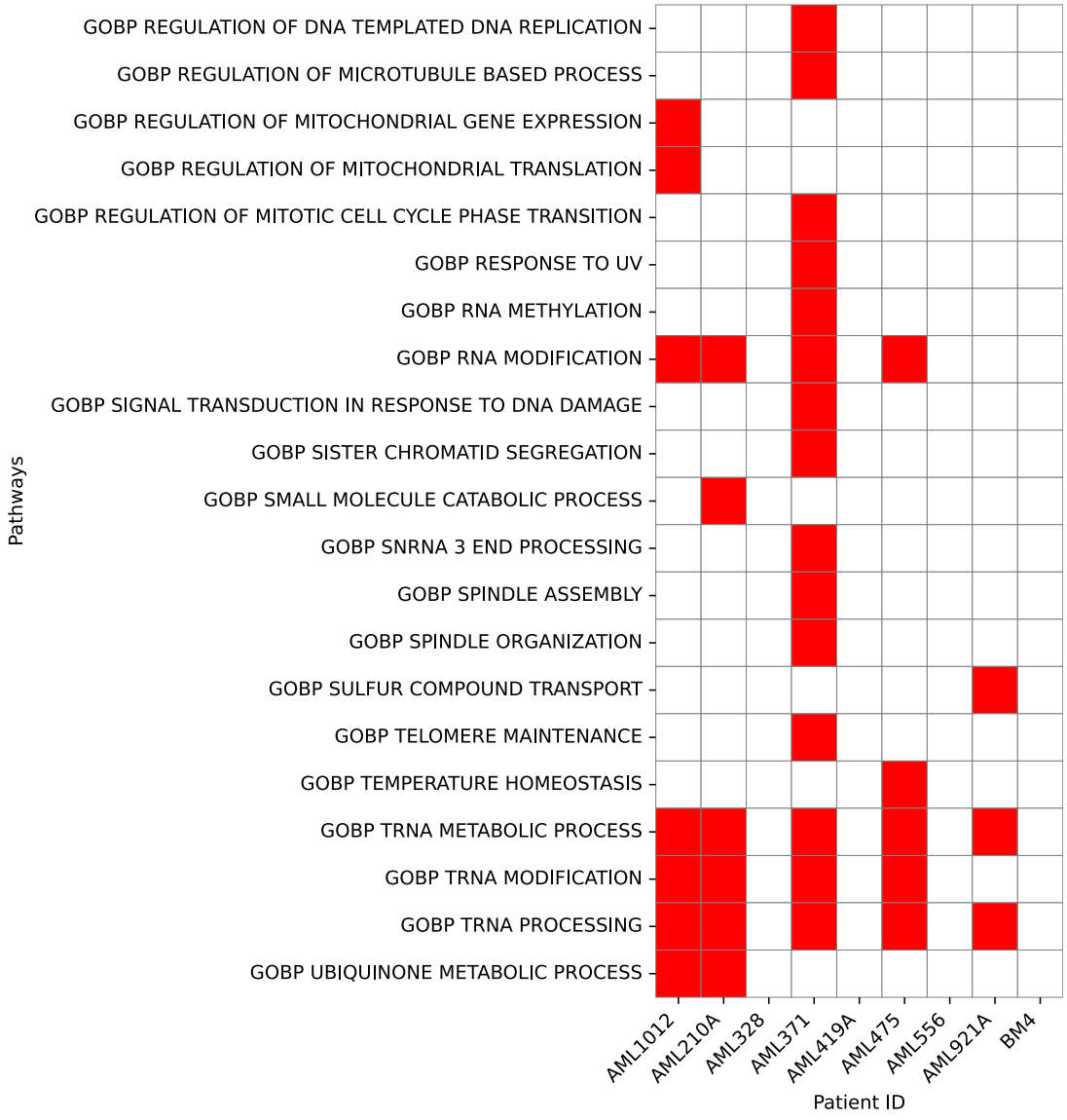

Figure 12: Gene Ontology Biological Process Pathway Enrichment of top 2500 genes by node degree/connections in monocyte cells for different patients (part 3 of 3). Benjamini-Hochberg correction was specified for multiple testing. Pathways with an adjusted p-value below 0.05 and q-value below 0.2 were considered significantly enriched.

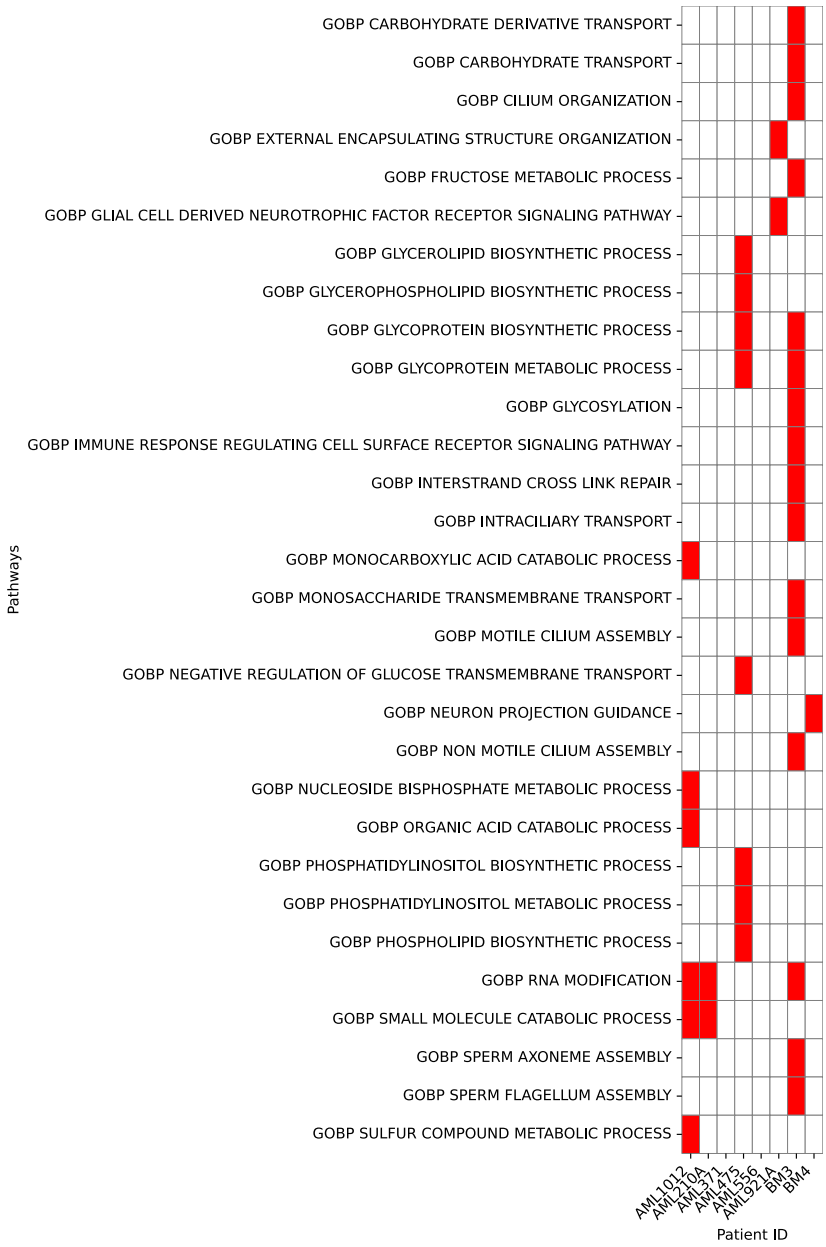

Figure 13: Gene Ontology Biological Process Pathway Enrichment of top 2500 genes by node degree/connections in dendritic cells for different patients (part 1 of 2). Benjamini-Hochberg correction was specified for multiple testing. Pathways with an adjusted p-value below 0.05 and q-value below 0.2 were considered significantly enriched.

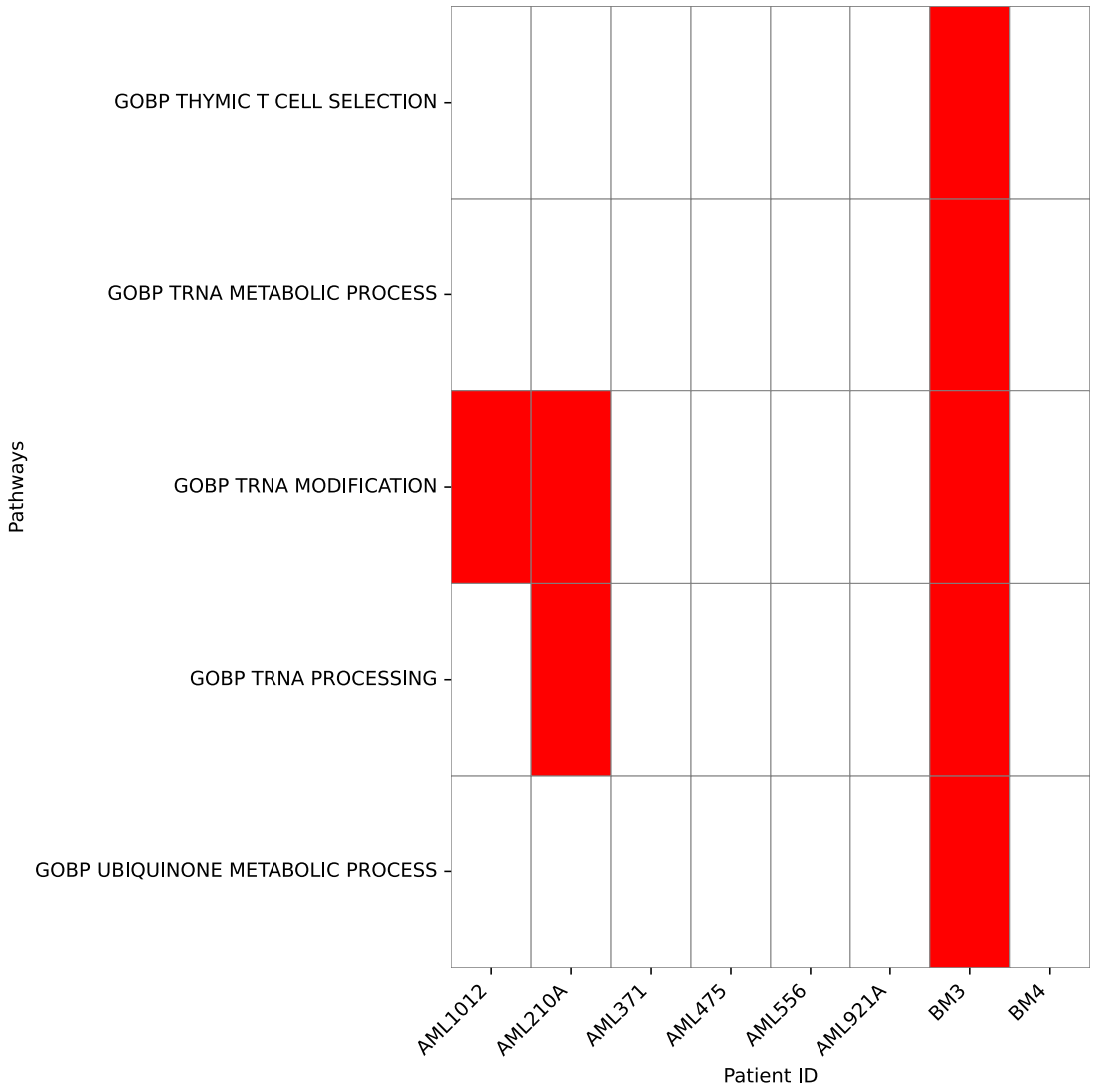

Figure 14: Gene Ontology Biological Process Pathway Enrichment of top 2500 genes by node degree/connections in dendritic cells for different patients (part 2 of 2). Benjamini-Hochberg correction was specified for multiple testing. Pathways with an adjusted p-value below 0.05 and q-value below 0.2 were considered significantly enriched.

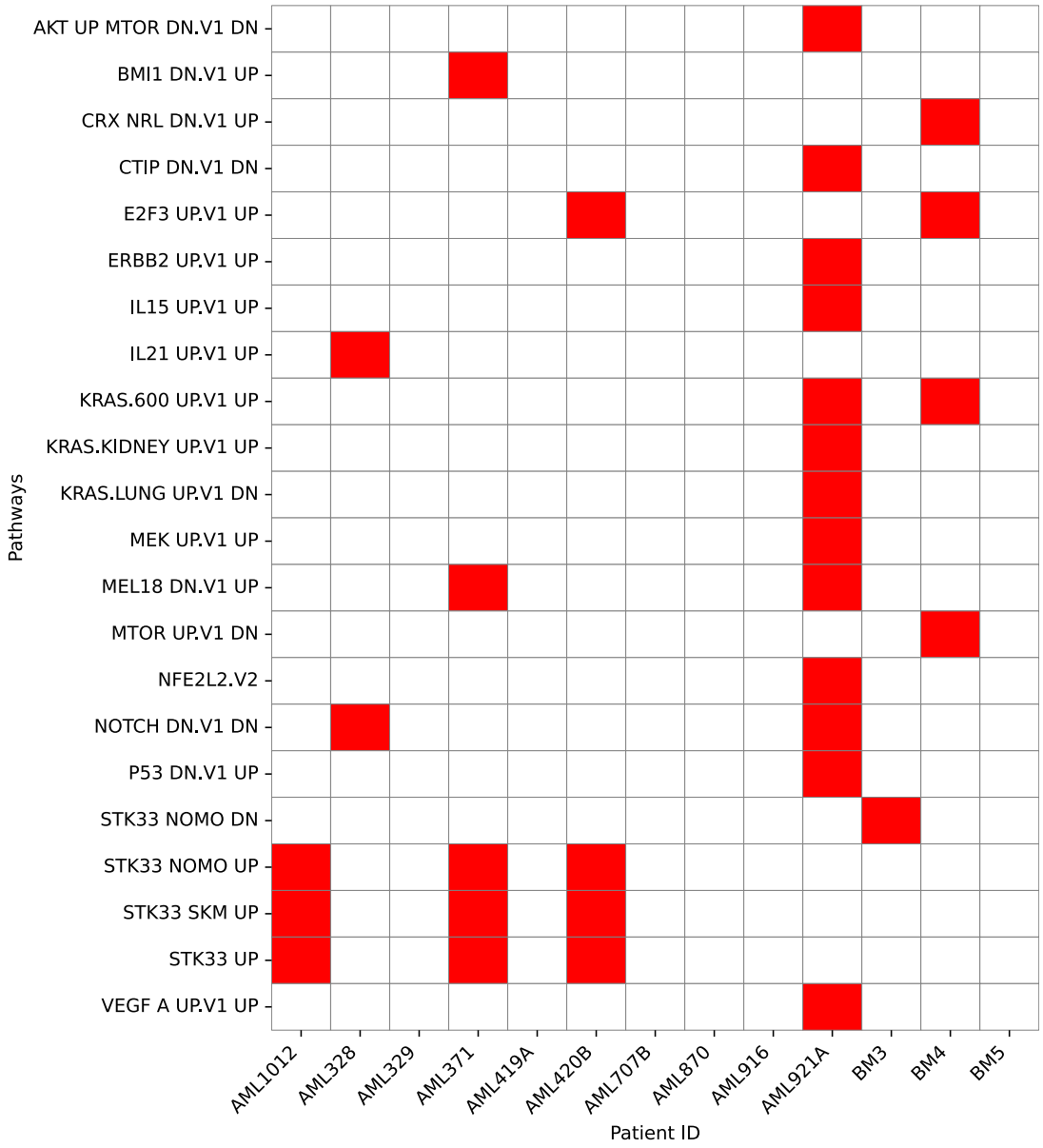

Figure 15: Oncogenic Signature Pathway Enrichment of top 2500 genes by node degree/connections in progenitor cells for different patients. Benjamini-Hochberg correction was specified for multiple testing. Pathways with an adjusted p-value below 0.05 and q-value below 0.2 were considered significantly enriched.

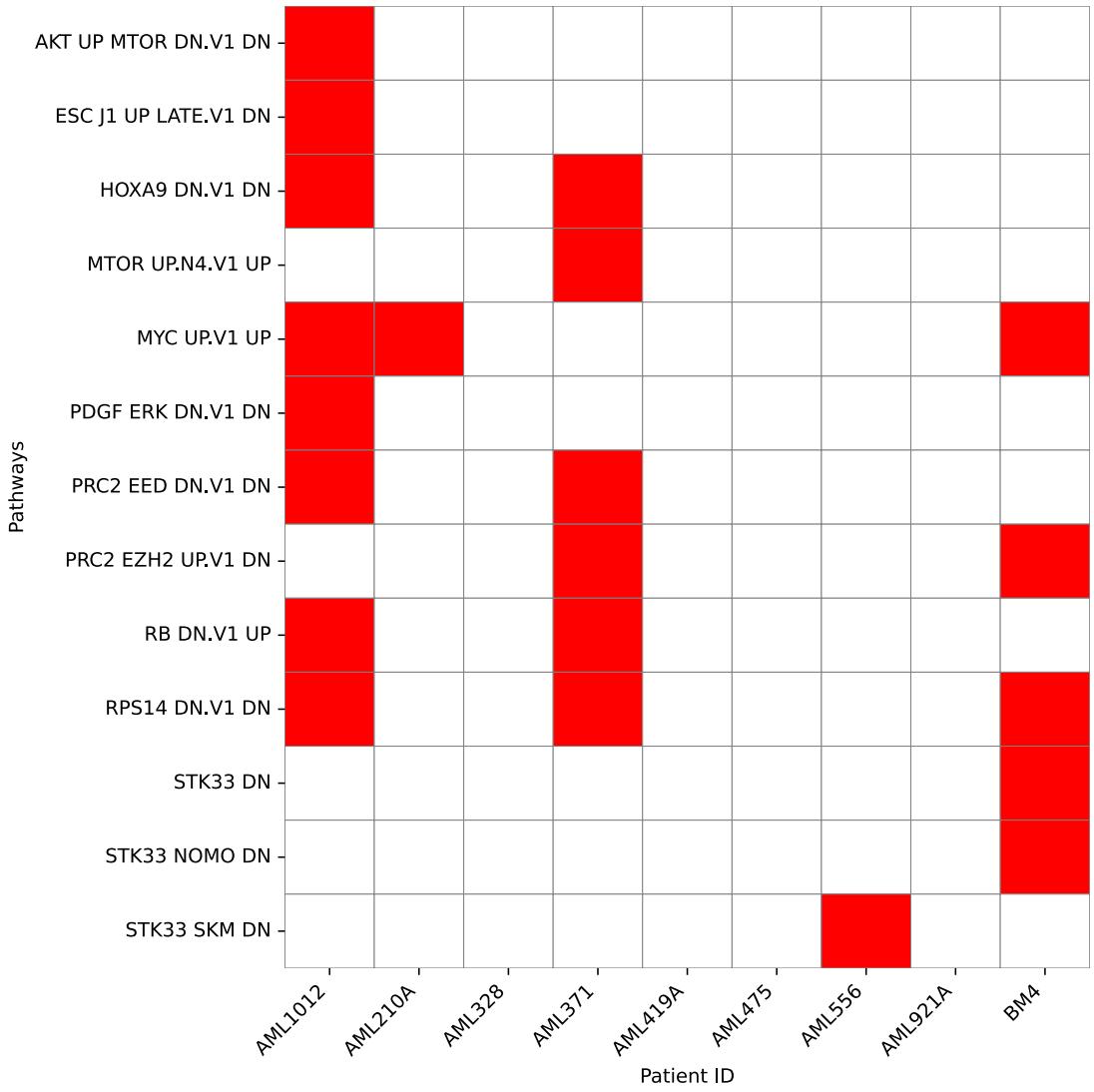

Figure 16: Oncogenic Signature Pathway Enrichment of top 2500 genes by node degree/connections in monocyte cells for different patients. Benjamini-Hochberg correction was specified for multiple testing. Pathways with an adjusted p-value below 0.05 and q-value below 0.2 were considered significantly enriched.